

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2003, 08:41:43 ; Search time 15 Seconds
(without alignments)
435.459 Million cell updates/sec

Title: US-09-508-710-2

Perfect score: 1173

Sequence: 1 MAGEKGLVLLDFWSPFQGR.....YSPDKVYDFIGLKKYKIE 222

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	857	73.1	224	2	US-08-924-759-22
2	857	73.1	224	3	US-09-248-335-22
3	818.5	69.8	225	2	US-08-924-759-12
4	818.5	69.8	225	3	US-09-248-335-12
5	683.5	58.3	219	3	US-08-924-747-6
6	683.5	58.3	219	4	US-09-296-715-6
7	681	58.1	218	4	US-09-247-373B-6
8	664.5	56.6	219	3	US-08-924-747-20
9	664.5	56.6	219	4	US-09-247-373B-20
10	664.5	56.6	219	4	US-09-296-715-20
11	639	54.5	216	3	US-08-924-747-12
12	639	54.5	216	4	US-09-247-373B-12
13	639	54.5	216	4	US-09-296-715-12
14	601.5	51.3	200	3	US-08-924-747-18
15	601.5	51.3	200	4	US-09-247-373B-18
16	601.5	51.3	200	4	US-09-296-715-18
17	566.5	48.3	221	4	US-09-247-373B-44
18	488	43.6	230	3	US-09-248-335-44
19	480	40.9	147	1	US-08-525-507-2
20	432.5	36.9	225	3	US-09-248-335-48
21	431.5	36.8	227	3	US-09-248-335-40
22	430	36.7	228	3	US-09-248-335-70
23	426.5	36.4	231	3	US-09-248-335-54
24	406	34.6	236	3	US-09-248-335-74
25	401	34.2	238	3	US-09-248-335-38
26	399.5	34.1	233	3	US-09-248-335-60
27	389.5	33.2	235	3	US-08-924-747-24

28	389.5	33.2	235	4	US-09-247-373B-24	Sequence 24, Appl
29	389.5	33.2	235	4	US-09-296-715-24	Sequence 24, Appl
30	383	32.7	240	3	US-09-248-335-42	Sequence 42, Appl
31	382.5	32.6	235	3	US-09-248-335-64	Sequence 64, Appl
32	380	32.4	236	3	US-09-248-335-68	Sequence 68, Appl
33	376.5	32.1	222	3	US-09-248-335-46	Sequence 46, Appl
34	374	31.9	227	3	US-09-248-335-66	Sequence 66, Appl
35	372.5	31.8	225	3	US-09-248-335-62	Sequence 62, Appl
36	370	31.5	232	3	US-09-248-335-56	Sequence 56, Appl
37	366	31.2	203	3	US-09-248-335-58	Sequence 58, Appl
38	365.5	31.2	234	3	US-09-248-335-52	Sequence 52, Appl
39	365	31.1	229	4	US-09-247-373B-48	Sequence 48, Appl
40	364	31.0	220	3	US-08-924-747-26	Sequence 26, Appl
41	364	31.0	220	4	US-09-247-373B-26	Sequence 26, Appl
42	364	31.0	220	4	US-09-296-715-26	Sequence 26, Appl
43	360.5	30.7	225	4	US-09-247-373B-36	Sequence 36, Appl
44	359.5	30.6	235	2	US-08-924-759-10	Sequence 10, Appl
45	359.5	30.6	235	3	US-09-248-335-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-924-759-22
; Sequence 22, Application US/08924759
; Patent No. 5962229
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: E.I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,759
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CL-1128
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: MAIZE
; IMMEDIATE SOURCE:
; CLONE: CEB5.PK0049.A11
US-08-924-759-22

Query Match 73.1%; Score 857; DB 2; Length 224;
Best Local Similarity 72.9%; Pred. No. 9, 7e-91;
Matches 164; Conservative 27; Mismatches 30; Indels 4; Gaps 3;

	Db	5	VULLDFWSPFGRVRIALAEKTEYFYKEEDL-RNKSPLLQMPVHKKTPVLTHNGKP	63
	QY	67	VNESLIITLYLEAFDPDAPALLSDPTARAQAQFWADVDKKVDCGSRINKLKGEPAQ	126
	Db	64	ISSESLAVQVITEEWNDRNFLPSDPTQRAQAQFWADVDIKIIDLGGKKIKTSGEKEA	123
	QY	127	ARAEMLDILKLPAGLDKPFPGDGKFGFDAAFPFTAWPHSYERGEFSULVAPAKIA	186
	Db	124	AKKEFEALKLEEQLGDKYFGGDNIGFVDIALVPFTWFVKVYETFGSLNIENECPRFV	183
	QY	187	AWAKRGERSVAKSLYSPDKVDTDFGLLKKKYIE	222
	Db	184	AWAKRCLQESVAKSLPDDQHKKVFVEFYVEIRKKLVIE	219

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RESULT 10
US-09-296-715-20
; Sequence 20, Application US/09296715
; Patent No. 6171839
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/296,715
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CL-1108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: SOYBEAN
; IMMEDIATE SOURCE:
; CLONE: SSL.PK0005.E6
US-09-296-715-20

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QY      127  ARAEMLDILTGALGDKPFPGDGKFGFVDAATAPETAWPHSYVERGEFSLPEVAKIA 186
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Db      124  AKFEIFALKLEQLGDKGYFGDNITGFVDIALVPFTTWPKVYETGSLNIENECPRFV 183
       : : : : : | : : | : | : | : | : | : | : | : | : | : | : | :
QY      187  AWAKRCGERESVAKSLSYSPDKVYDFIGLKKKYGIE 222
       : : : : : | : : | : | : | : | : | : | : | : | : | : | : | :
Db      184  AWAKRCLQKESVAKSLPDQHVKVYEVVEIRKKLVIE 219
       : : : : : | : : | : | : | : | : | : | : | : | : | : | : | :

RESULT 11
US-08-924-747-12
; Sequence 12, Application US/08924747
; Patent No. 6063570
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,747
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CL-1108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 216 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; ORIGINAL SOURCE: SOYBEAN
; TISSUE TYPE: SOYBEAN
; IMMEDIATE SOURCE:
; CLONE: SEG.PK0048.D7
US-08-924-747-12

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Query Match	54.5%;	Score 639;	DB 3;	Length 216;
Best Local Similarity	55.9%;	Pred. No. 1.2e-65;		
Matches 124;	Conservative 33;	Mismatches 59;	Indels 6;	Gaps 3;
QY	1	MAGEKGLVLDFWSPFGQVRVRLTAALAEKGLPYABEDLMAGKSDRLLRANPVHKKIPVL	60	
Db		:		
	1	MADE--VLLDFWSPFGQVRVRLTAALAEKGIKYESKEEDLQ-NKSPLLAKMNPVHKKIPVL	57	
QY	61	LHDGRAVNSLIITQYLEAFDPAPALLSDPYARAQARFWADYVDKYYDCGSRLLWLK	120	
Db		: : : : : :		
	58	IUNGPICSILVAVQYIEEVNDNRNPLSDPYQRAQARFWADFYVDKIFDLGRKIWTSK	117	
QY	121	GPQQAARAEMLDILKTLDGALGDKPFGFGDKFGFYDAAFPATMFHVSRYGERSLPE	180	
Db		: : : :		
	118	GEEKAAKKEFTEALKLEEQLGDKTYFGDDLDLGFVDIALIFDFTWF---KTFGSUNIES	174	
QY	181	VAPKTAAWAKRCGRSVAKSLSPDKYDFDTGLLAKKYGIE	222	
		: : :		

Db 175 ECPKFVAAKRLQKDSVAKSLPDQHKVYEFIMDKKFDIE 216

RESULT 12

US-09-247-373B-12

Sequence 12, Application US/09247373B

Patent No. 6168954

GENERAL INFORMATION:

APPLICANT: MCGONIGLE, BRIAN

APPLICANT: O'KEEFE, DANIEL

TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES

FILE REFERENCE: CL-1108-A

CURRENT APPLICATION NUMBER: US/09/247,373B

CURRENT FILING DATE: 1999-02-10

PRIOR APPLICATION NUMBER: 08/924,747

PRIOR FILING DATE: 1997-09-05

NUMBER OF SEQ ID NOS: 56

SOFTWARE: Microsoft Office 97

SEQ ID NO 12

LENGTH: 216

TYPE: PRT

ORGANISM: SOYBEAN

US-09-247-373B-12

Query Match 54.5%; Score 639; DB 4; Length 216;

Best Local Similarity 55.9%; Pred. No. 1.2e-65;

Matches 124; Conservative 33; Mismatches 59; Indels 6; Gaps 3;

QY 1 MAGEKGLVLDFWVSPFGQVRVIALAEKGLPYEAEEDLMAGKSDRLLRANPVHKKIPVL 60

Db 1 MADE--VLLDFWVSPFGMRVIALAEKGIKYESKEEDLQ--NKSPLLKMPVHKKIPVL 57

QY 61 LHGRVAVNESLILOYLEEAFDPAPALLPSDPYARAQAFWADYVDKVVDCGSLWLKL 120

Db 58 IHNGKPCISLVAQVIEEVDNRNPLPSDPYQRAQAFWADVDNKFIDLGRKIWTSK 117

QY 121 GEQAQARAEMLDILKTLGALGDKPFFGDKFGFVDAFAFPTAFWHSYERYGFSPLPE 180

Db 118 GEEKAARKFEIALKEQLGDKTYFGDDLGFDVIALIPDTWF---KTFGSLNIES 174

QY 181 VAPKIAAAKRCGERESVAKSLYSPDKVYDFIGLLKKYKIE 222

Db 175 ECPKFVAAKRLQKDSVAKSLPDQHKVYEFIMDKKFDIE 216

RESULT 13

US-09-296-715-12

Sequence 12, Application US/09296715

Patent No. 6171839

GENERAL INFORMATION:

APPLICANT: MCGONIGLE, BRIAN

APPLICANT: O'KEEFE, DANIEL

TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE

TITLE OF INVENTION: ENZYMES

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

STATE: DELAWARE

COUNTRY: UNITED STATES OF AMERICA

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95

SOFTWARE: MICROSOFT WORD VERSION 7.0A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/296,715

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: FLOYD, LINDA AXAMETHY

REGISTRATION NUMBER: 33,692

REFERENCE/DOCKET NUMBER: CL-1108

TELEPHONE: 302-892-8112

TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 18:

Db 175 ECPKFVAAKRLQKDSVAKSLPDQHKVYEFIMDKKFDIE 216

US-09-247-373B-12

Query Match 54.5%; Score 639; DB 4; Length 216;

Best Local Similarity 55.9%; Pred. No. 1.2e-65;

Matches 124; Conservative 33; Mismatches 59; Indels 6; Gaps 3;

QY 1 MAGEKGLVLDFWVSPFGQVRVIALAEKGLPYEAEEDLMAGKSDRLLRANPVHKKIPVL 60

Db 1 MADE--VLLDFWVSPFGMRVIALAEKGIKYESKEEDLQ--NKSPLLKMPVHKKIPVL 57

QY 61 LHGRVAVNESLILOYLEEAFDPAPALLPSDPYARAQAFWADYVDKVVDCGSLWLKL 120

Db 58 IHNGKPCISLVAQVIEEVDNRNPLPSDPYQRAQAFWADVDNKFIDLGRKIWTSK 117

QY 121 GEQAQARAEMLDILKTLGALGDKPFFGDKFGFVDAFAFPTAFWHSYERYGFSPLPE 180

Db 118 GEEKAARKFEIALKEQLGDKTYFGDDLGFDVIALIPDTWF---KTFGSLNIES 174

QY 181 VAPKIAAAKRCGERESVAKSLYSPDKVYDFIGLLKKYKIE 222

Db 175 ECPKFVAAKRLQKDSVAKSLPDQHKVYEFIMDKKFDIE 216

US-09-296-715-12

Query Match 54.5%; Score 639; DB 4; Length 216;

Best Local Similarity 55.9%; Pred. No. 1.2e-65;

Matches 124; Conservative 33; Mismatches 59; Indels 6; Gaps 3;

QY 1 MAGEKGLVLDFWVSPFGQVRVIALAEKGLPYEAEEDLMAGKSDRLLRANPVHKKIPVL 60

Db 1 MADE--VLLDFWVSPFGMRVIALAEKGIKYESKEEDLQ--NKSPLLKMPVHKKIPVL 57

QY 61 LHGRVAVNESLILOYLEEAFDPAPALLPSDPYARAQAFWADYVDKVVDCGSLWLKL 120

Db 58 IHNGKPCISLVAQVIEEVDNRNPLPSDPYQRAQAFWADVDNKFIDLGRKIWTSK 117

QY 121 GEQAQARAEMLDILKTLGALGDKPFFGDKFGFVDAFAFPTAFWHSYERYGFSPLPE 180

Db 118 GEEKAARKFEIALKEQLGDKTYFGDDLGFDVIALIPDTWF---KTFGSLNIES 174

QY 181 VAPKIAAAKRCGERESVAKSLYSPDKVYDFIGLLKKYKIE 222

Db 175 ECPKFVAAKRLQKDSVAKSLPDQHKVYEFIMDKKFDIE 216

US-09-296-715-12

Query Match 54.5%; Score 639; DB 4; Length 216;

Best Local Similarity 55.9%; Pred. No. 1.2e-65;

Matches 124; Conservative 33; Mismatches 59; Indels 6; Gaps 3;

QY 1 MAGEKGLVLDFWVSPFGQVRVIALAEKGLPYEAEEDLMAGKSDRLLRANPVHKKIPVL 60

Db 1 MADE--VLLDFWVSPFGMRVIALAEKGIKYESKEEDLQ--NKSPLLKMPVHKKIPVL 57

QY 61 LHGRVAVNESLILOYLEEAFDPAPALLPSDPYARAQAFWADYVDKVVDCGSLWLKL 120

Db 58 IHNGKPCISLVAQVIEEVDNRNPLPSDPYQRAQAFWADVDNKFIDLGRKIWTSK 117

QY 121 GEQAQARAEMLDILKTLGALGDKPFFGDKFGFVDAFAFPTAFWHSYERYGFSPLPE 180

Db 118 GEEKAARKFEIALKEQLGDKTYFGDDLGFDVIALIPDTWF---KTFGSLNIES 174

QY 181 VAPKIAAAKRCGERESVAKSLYSPDKVYDFIGLLKKYKIE 222

Db 175 ECPKFVAAKRLQKDSVAKSLPDQHKVYEFIMDKKFDIE 216

US-09-296-715-12

Query Match 54.5%; Score 639; DB 4; Length 216;

Best Local Similarity 55.9%; Pred. No. 1.2e-65;

Matches 124; Conservative 33; Mismatches 59; Indels 6; Gaps 3;

QY 1 MAGEKGLVLDFWVSPFGQVRVIALAEKGLPYEAEEDLMAGKSDRLLRANPVHKKIPVL 60

Db 1 MADE--VLLDFWVSPFGMRVIALAEKGIKYESKEEDLQ--NKSPLLKMPVHKKIPVL 57

QY 61 LHGRVAVNESLILOYLEEAFDPAPALLPSDPYARAQAFWADYVDKVVDCGSLWLKL 120

Db 58 IHNGKPCISLVAQVIEEVDNRNPLPSDPYQRAQAFWADVDNKFIDLGRKIWTSK 117

QY 121 GEQAQARAEMLDILKTLGALGDKPFFGDKFGFVDAFAFPTAFWHSYERYGFSPLPE 180

Db 118 GEEKAARKFEIALKEQLGDKTYFGDDLGFDVIALIPDTWF---KTFGSLNIES 174

QY 181 VAPKIAAAKRCGERESVAKSLYSPDKVYDFIGLLKKYKIE 222

Db 175 ECPKFVAAKRLQKDSVAKSLPDQHKVYEFIMDKKFDIE 216

US-09-296-715-12

Query Match 54.5%; Score 639; DB 4; Length 216;

Best Local Similarity 55.9%; Pred. No. 1.2e-65;

Matches 124; Conservative 33; Mismatches 59; Indels 6; Gaps 3;

QY 1 MAGEKGLVLDFWVSPFGQVRVIALAEKGLPYEAEEDLMAGKSDRLLRANPVHKKIPVL 60

Db 1 MADE--VLLDFWVSPFGMRVIALAEKGIKYESKEEDLQ--NKSPLLKMPVHKKIPVL 57

QY 61 LHGRVAVNESLILOYLEEAFDPAPALLPSDPYARAQAFWADYVDKVVDCGSLWLKL 120

Db 58 IHNGKPCISLVAQVIEEVDNRNPLPSDPYQRAQAFWADVDNKFIDLGRKIWTSK 117

QY 121 GEQAQARAEMLDILKTLGALGDKPFFGDKFGFVDAFAFPTAFWHSYERYGFSPLPE 180

Db 118 GEEKAARKFEIALKEQLGDKTYFGDDLGFDVIALIPDTWF---KTFGSLNIES 174

QY 181 VAPKIAAAKRCGERESVAKSLYSPDKVYDFIGLLKKYKIE 222

Db 175 ECPKFVAAKRLQKDSVAKSLPDQHKVYEFIMDKKFDIE 216

US-09-296-715-12

Query Match 54.5%; Score 639; DB 4; Length 216;

Best Local Similarity 55.9%; Pred. No. 1.2e-65;

Matches 124; Conservative 33; Mismatches 59; Indels 6; Gaps 3;

QY 1 MAGEKGLVLDFWVSPFGQVRVIALAEKGLPYEAEEDLMAGKSDRLLRANPVHKKIPVL 60

Db 1 MADE--VLLDFWVSPFGMRVIALAEKGIKYESKEEDLQ--NKSPLLKMPVHKKIPVL 57

QY 61 LHGRVAVNESLILOYLEEAFDPAPALLPSDPYARAQAFWADYVDKVVDCGSLWLKL 120

Db 58 IHNGKPCISLVAQVIEEVDNRNPLPSDPYQRAQAFWADVDNKFIDLGRKIWTSK 117

QY 121 GEQAQARAEMLDILKTLGALGDKPFFGDKFGFVDAFAFPTAFWHSYERYGFSPLPE 180

Db 118 GEEKAARKFEIALKEQLGDKTYFGDDLGFDVIALIPDTWF---KTFGSLNIES 174

QY 181 VAPKIAAAKRCGERESVAKSLYSPDKVYDFIGLLKKYKIE 222

Db 175 ECPKFVAAKRLQKDSVAKSLPDQHKVYEFIMDKKFDIE 216

US-09-296-715-12

Query Match 54.5%; Score 639; DB 4; Length 216;

Best Local Similarity

Db 175 ECPKFVAAKRLQKDSVAKSLPDQHKVYEFIMDRKKFDIE 216

RESULT 12

US-09-247-373B-12

Sequence 12, Application US/09247373B

Patent No. 6168954

GENERAL INFORMATION:

APPLICANT: MCGONIGLE, BRIAN

APPLICANT: O'KEEFE, DANIEL

TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES

FILE REFERENCE: CL-1108-A

CURRENT APPLICATION NUMBER: US/09/247,373B

CURRENT FILING DATE: 1999-02-10

PRIOR APPLICATION NUMBER: 08/924,747

PRIOR FILING DATE: 1997-09-05

NUMBER OF SEQ ID NOS: 56

SOFTWARE: Microsoft Office 97

SEQ ID NO 12

LENGTH: 216

TYPE: PRT

ORGANISM: SOYBEAN

US-09-247-373B-12

Query Match 54.5%; Score 639; DB 4; Length 216;

Best Local Similarity 55.9%; Pred. No. 1.2e-65;

Matches 124; Conservative 33; Mismatches 59; Indels 6; Gaps 3;

QY 1 MAGEKGLVLDFWVSPFGQVRVIALAEKGLPYEAEEDLMAGKSDRLLRANPVHKKIPVL 60

Db 1 MADE--VLLDFWSPFGMRVIALAEKGIKYESKEEDLQ--NKSPLLKMPVHKKIPVL 57

QY 61 LHGRVAVNESLILOYLEEAFDPAPALLPSDPYARAQAFWADYDKKVDGSGSLWLK 120

Db 58 IHNGKPCISLVAQVIEEVDNRNPLPSDPYQRAQAFWADVDNKFIDLGRKIWTSK 117

QY 121 GEQAQARAEMLDILKTLGALGDKPFFGDKFGFVDAAFAFPTAFWHSYERYGFSLPE 180

Db 118 GEEKAKEFEIALKEELQGLDKTYFGDDLGFDVIALIPDTWF---KTFGSLNIES 174

QY 181 VAPKIAAAKRCGERESVAKSLYSPDKVYDFIGLLKKYKIE 222

Db 175 ECPKFVAAKRLQKDSVAKSLPDQHKVYEFIMDRKKFDIE 216

RESULT 13

US-09-296-715-12

Sequence 12, Application US/09296715

Patent No. 6171839

GENERAL INFORMATION:

APPLICANT: MCGONIGLE, BRIAN

APPLICANT: O'KEEFE, DANIEL

TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE

TITLE OF INVENTION: ENZYMES

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

STATE: DELAWARE

COUNTRY: UNITED STATES OF AMERICA

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95

SOFTWARE: MICROSOFT WORD VERSION 7.0A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/296,715

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: FLOYD, LINDA AXAMETHY

REGISTRATION NUMBER: 33,692

REFERENCE/DOCKET NUMBER: CL-1108

TELEPHONE: 302-892-8112

TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 18:

Db 175 ECPKFVAAKRLQKDSVAKSLPDQHKVYEFIMDRKKFDIE 216

Search completed: July 1, 2003, 09:00:58
Job time : 16 secs

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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 200 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ TISSUE TYPE: SOYBEAN
/ IMMEDIATE SOURCE:
/ CLONE: SSL.PK0002.F7
US-08-924-747-18

Query Match      51.3%; Score 601.5; DB 3; Length 200;
Best Local Similarity 55.3%; Pred. No. 2.2e-61;
Matches 109; Conservative 32; Mismatches 55; Indels 1; Gaps 1;

QY      6 GLVLLDFWSPGQVRIRIALAEKGLPEYEAEDLMAGKSDRLLRANPVHKKIPVLLHGR 65
Db      4 GVYLLDTWASFMGMRVIRIALAEKGVYEYKEENL-RNKSPLLQMNPIHKKIPVLIHNG 62
QY      66 AVNESLTIQLYLEAFDPDAPALLPSDPYARAQARFWADYVKKVYDCGSRLLWKLKGEPPQA 125
Db      63 PICESAIIVQYIDEVWNDKAPILPSDPYERAQARFWYDIDKKVYDTWRKMWLSKGEHE 122
QY      126 QARAEMLDILKTLDGALGDKPFFGDKFGFVDAAFAPFTAWFHSHYERYGEFSLPEVAPKI 185
Db      123 AGKKEFISIFKQLEETLSDKAYGSDTFGLDIGLIPFYSWFYTFETYGNFKMEECPCPL 182
QY      186 AAWAKRCGERESVAKSL 202
Db      183 VAWAKRCMQREAVSKSL 199

RESULT 15
US-09-247-373B-18
/ Sequence 18, Application US/09247373B
/ Patent No. 6188954
/ GENERAL INFORMATION:
/ APPLICANT: MCGONIGLE, BRIAN
/ APPLICANT: O'KEEFE, DANIEL
/ TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
/ FILE REFERENCE: CL-1108-A
/ CURRENT APPLICATION NUMBER: US/09/247,373B
/ PRIOR FILING DATE: 1999-02-10
/ PRIOR APPLICATION NUMBER: 08/924,747
/ PRIOR FILING DATE: 1997-09-05
/ NUMBER OF SEQ ID NOS: 56
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 18
/ LENGTH: 200
/ TYPE: PRT
/ ORGANISM: SOYBEAN
US-09-247-373B-18

Query Match      51.3%; Score 601.5; DB 4; Length 200;
Best Local Similarity 55.3%; Pred. No. 2.2e-61;
Matches 109; Conservative 32; Mismatches 55; Indels 1; Gaps 1;

QY      6 GLVLLDFWSPGQVRIRIALAEKGLPEYEAEDLMAGKSDRLLRANPVHKKIPVLLHGR 65
Db      4 GVYLLDTWASFMGMRVIRIALAEKGVYEYKEENL-RNKSPLLQMNPIHKKIPVLIHNG 62
QY      66 AVNESLTIQLYLEAFDPDAPALLPSDPYARAQARFWADYVKKVYDCGSRLLWKLKGEPPQA 125
Db      63 PICESAIIVQYIDEVWNDKAPILPSDPYERAQARFWYDIDKKVYDTWRKMWLSKGEHE 122
QY      126 QARAEMLDILKTLDGALGDKPFFGDKFGFVDAAFAPFTAWFHSHYERYGEFSLPEVAPKI 185
Db      123 AGKKEFISIFKQLEETLSDKAYGSDTFGLDIGLIPFYSWFYTFETYGNFKMEECPCPL 182
QY      186 AAWAKRCGERESVAKSL 202
Db      183 VAWAKRCMQREAVSKSL 199
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OM protein - protein search, using sw model

Run on: July 1, 2003, 08:53:35 ; Search time 21 Seconds
(without alignments)
1159.124 Million cell updates/sec

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Perfect score: 1173
Sequence: 1 MAGEKGLVLDWFVSPFQGR.....YSPDKVYDFIGLLKKYKIE 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 424699 seqs, 109646833 residues
Total number of hits satisfying chosen parameters: 424699

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	405.5	34.6	236	10 US-09-765-213A-9	Sequence 9, Appli
2	362.5	30.9	229	10 US-09-765-213A-8	Sequence 8, Appli
3	334	28.5	233	10 US-09-765-213A-2	Sequence 2, Appli
4	331.5	28.3	225	10 US-09-765-213A-7	Sequence 7, Appli
5	320.5	27.3	224	10 US-09-765-213A-11	Sequence 11, Appli
6	319	27.2	233	10 US-09-765-213A-4	Sequence 4, Appli
7	309	26.3	233	10 US-09-765-213A-6	Sequence 6, Appli
8	291	24.8	240	10 US-09-765-213A-10	Sequence 10, Appli
9	235	20.0	83	10 US-09-050-010-7	Sequence 7, Appli
10	198	16.9	212	10 US-09-741-669-351	Sequence 351, App
11	172.5	14.7	241	9 US-09-854-133-194	Sequence 194, App
12	172.5	14.7	241	9 US-10-225-273-4	Sequence 4, Appli
13	172.5	14.7	241	10 US-09-738-973-194	Sequence 194, App
14	172.5	14.7	286	10 US-09-925-302-653	Sequence 653, App
15	167.5	14.3	241	9 US-09-854-133-204	Sequence 204, App
16	167.5	14.3	241	10 US-09-738-973-204	Sequence 204, App
17	129.5	11.0	86	10 US-09-050-010-6	Sequence 6, Appli
18	124	10.6	195	9 US-09-798-889-164	Sequence 164, App
19	121.5	10.4	263	9 US-09-769-787-68	Sequence 68, Appli

20	110	9.4	240	9 US-09-964-899-23	Sequence 23, Appli
21	102	8.7	461	9 US-10-106-698-4705	Sequence 4705, Ap
22	101	8.6	354	10 US-09-801-368-414	Sequence 414, App
23	99	8.4	255	10 US-09-925-297-761	Sequence 761, App
24	94	8.0	367	10 US-09-731-872-395	Sequence 395, App
25	94	8.0	367	10 US-09-731-872-403	Sequence 403, App
26	87	7.4	229	9 US-10-102-806-554	Sequence 554, App
27	81	6.9	345	9 US-10-047-260-34	Sequence 34, Appli
28	78.5	6.7	436	10 US-09-925-301-928	Sequence 928, App
29	78	6.6	839	9 US-10-231-035-6	Sequence 6, Appli
30	77.5	6.6	555	10 US-09-801-368-350	Sequence 350, App
31	75	6.4	141	9 US-09-796-692-1310	Sequence 1310, Ap
32	75	6.4	141	9 US-09-796-692-1783	Sequence 1783, Ap
33	75	6.4	141	9 US-09-796-692-2051	Sequence 2051, Ap
34	75	6.4	141	9 US-09-796-692-2301	Sequence 2301, Ap
35	75	6.4	141	9 US-10-040-862-1310	Sequence 1310, Ap
36	75	6.4	141	9 US-10-040-862-1783	Sequence 1783, Ap
37	75	6.4	141	9 US-10-040-862-2051	Sequence 2051, Ap
38	75	6.4	141	9 US-10-040-862-2301	Sequence 2301, Ap
39	74.5	6.4	390	10 US-09-925-300-1649	Sequence 1649, Ap
40	74.5	6.4	417	9 US-10-305-348-8	Sequence 8, Appli
41	74.5	6.4	442	9 US-10-072-036-127	Sequence 127, App
42	74.5	6.4	570	10 US-09-877-633-13	Sequence 13, Appli
43	74.5	6.4	570	10 US-09-877-633-14	Sequence 14, Appli
44	74	6.3	513	10 US-09-833-745-55	Sequence 55, Appli
45	73.5	6.3	256	9 US-09-981-876-180	Sequence 180, App

ALIGNMENTS

RESULT 1
US-09-765-213A-9
; Sequence 9 Application US/09765213A
; Patent No. US20020079846A1
; GENERAL INFORMATION:
; APPLICANT: Facchini, Peter J
; TITLE OF INVENTION: NO. US20020079846A1e1 Glutathione-S-Transferase Nucleic Acids
; FILE OF INVENTION: Polypeptides and Methods of Use
; FILE REFERENCE: 22542-001
; CURRENT APPLICATION NUMBER: US/09/765,213A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/176708
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ IDS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; TYPE: PRT
; ORGANISM: Picea mariana
US-09-765-213A-9

Query Match 34.6%; Score 405.5; DB 10; Length 236;
Best Local Similarity 42.3%; Pred. No. 7.5e-35;
Matches 96; Conservative 40; Mismatches 80; Indels 11; Gaps 5;
QY 3 GEKGLV-LIDFWVSPFGQVRVIALAEKGLPYEAEDLMAGKSDRLLRANPVHKIPVLL 61
Db 5 GEAKVLLGGNISPFVLRVIALALGIDYEFIEEN-MONKSHLLQSNPVNKKIPVLI 63
QY 62 HDGRAVNESLIIQYLEAF-PDAPALLPSDPYARAQARFWADYDKVYDCGSRWLK 120
Db 64 HNGKPVCSNIIQYIDEAWDKAPVLMKPDYDRAIRFAAFVDDKLLPCLRGVFKQ 123
QY 121 GEPQAQARMELDKLTLDGAL-----GDKPFGGDKFGVDAAFPAPTFAMFHSYRG 174
Db 124 GEQQAKALESGASFTLLLEALNTSHCFSGKPPVFGGDEIGFLDIALGGMLAFVKALEYT 183
QY 175 EFSL--PFVAPKTAWAKRCGERESVAKSLYSPDKYDFIGLLKKY 219
Db 184 NLVLIDQEKPLLSLTMNRFCEADGVKMDPDPKLEQFISAIRVF 230


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RESULT 2
US-09-765-213A-8
; Sequence 8, Application US/09765213A
; Patent No. US20020079846A1
; GENERAL INFORMATION:
; APPLICANT: Facchini, Peter J
; TITLE OF INVENTION: No. US20020079846A1e1 Glutathione-S-Transferase Nucleic Acids and
; TITLE OF INVENTION: Polypeptides and Methods of Use
; FILE REFERENCE: 22542-001
; CURRENT APPLICATION NUMBER: US/09/765,213A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/176708
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Aegilops squarrosa
US-09-765-213A-8

Query Match      30.9%; Score 362.5; DB 10; Length 229;
Best Local Similarity 42.3%; Pred. No. 2.5e-30;
Matches 93; Conservative 33; Mismatches 79; Indels 15; Gaps 8;

QY 2 AGEKGLVLDFWVSPFGQVRVIALAEKGLPYEAEDLMAGKSDRLLRANPVHKKIPVLL 61
Db 3 AGGDDLKLLGANPSPVTRVKLALAKGLSYEDVEDLYK-KSELLKSNPVHKKIPVLI 61
QY 62 HGRVAVNESLIIQYLEEAFPPD-APALLSPDYARAQARFWADYDKVYDCGSRLLWKL 120
Db 62 HNGAPVCESNIIQYIDYFVFASTGPSLLPADPYERAIRFWAVDDKLV--APWRQW-LR 118
QY 121 G---EPQQAARAEMLDILKALGD----KPFPGDGFVDAAPFTAFWPHSYEY 173
Db 119 GTEEEKSGKQAFVAAVGEALRECKSGGGFGDGVG-LDVAGLVLSMMKVTEAL 177
QY 174 GFSLPEVA--PKIAAWAKRCGERESVAKSLYSPDKVYDF 211
Db 178 SGDKIFDAKTPLLAAWVERFELDRAKAALPDVGRLEEF 217

RESULT 3
US-09-765-213A-2
; Sequence 2, Application US/09765213A
; Patent No. US20020079846A1
; GENERAL INFORMATION:
; APPLICANT: Facchini, Peter J
; TITLE OF INVENTION: No. US20020079846A1e1 Glutathione-S-Transferase Nucleic Acids and
; TITLE OF INVENTION: Polypeptides and Methods of Use
; FILE REFERENCE: 22542-001
; CURRENT APPLICATION NUMBER: US/09/765,213A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/176708
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Papaver somniferum
US-09-765-213A-2

Query Match      28.5%; Score 334; DB 10; Length 233;
Best Local Similarity 35.1%; Pred. No. 2.7e-27;
Matches 81; Conservative 42; Mismatches 88; Indels 20; Gaps 7;

QY 2 AGEKGLVLDFWVSPFGQVRVIALAEKGLPYEAEDLMAGKSDRLLRANPVHKKIPVLL 61
Db 4 SGSEEVKILGGFSPFVMPRPNALNKSVKY-YLLEETFGSKSELLKSNPIYKRPVLI 62
QY 62 HGRVAVNESLIIQYLEEAFPPD-PALLSPDYARAQARFWADYDKVYDCGSRLLWKL 120
Db 62 HGRVAVNESLIIQYLEEAFPPD-PALLSPDYARAQARFWADYDKVYDCGSRLLWKL 120

Db 63 HGDKPICESMIIVQYIDYVWASAGHSIIIPSDPYDASIAFWATYIDDKFPFSLMGIAKSK 122
QY 121 GEPOQAARAEM-----LDIL-----KTLDGALGDKPFGGDKFGVDAAFPATFPHSYE 171
Db 123 DAEKKAALAEQAIAAFGILAEAYQTSKG-----KDFGGEKIGYVDIAFGCVGVIRVTE 178
QY 172 RYGEFSL--PEVAPKIAAWAKRCGERESVAKSLYSPDKVYDFIGLLKKKYG 220
Db 179 KMGIKLFDEEKVPGLTKWAERFCADETKVSVMPTDALMEF---AKKIFG 226

RESULT 4
US-09-765-213A-7
; Sequence 7, Application US/09765213A
; Patent No. US20020079846A1
; GENERAL INFORMATION:
; APPLICANT: Facchini, Peter J
; TITLE OF INVENTION: No. US20020079846A1e1 Glutathione-S-Transferase Nucleic Acids
; TITLE OF INVENTION: Polypeptides and Methods of Use
; FILE REFERENCE: 22542-001
; CURRENT APPLICATION NUMBER: US/09/765,213A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/176708
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-765-213A-7

Query Match      28.3%; Score 331.5; DB 10; Length 225;
Best Local Similarity 34.7%; Pred. No. 4.7e-27;
Matches 82; Conservative 46; Mismatches 83; Indels 25; Gaps 9;

QY 1 MAGEKGLVLDFWVSPFGQVRVIALAEKGLPYEAEE-DLMAGKSDRLLRANPVHKKIPV 59
Db 1 MAQNTVTLIGSWSSPYSILRAVVALHLSVKVEYLDLDPVLKEKSELLKSNPIHKKVPV 60
QY 60 LLHGRVAVNESLIIQYLEEAFPPDAPALLSPDYARAQARFWADYDKVYDCGSRLLWKL 119
Db 61 LLHGDLSISESLNVVQY-DEAWPSVPSILPSDAYDRASARFWAQIDDK---CFAAVDAV 115
QY 120 KG-----EPQQAARAEMLDILKILD-----GALGDKPFGGDKFGVDAAFPATFPH 168
Db 116 VGAKDDEGKMAAVGKLMECLAILEETFKSSKGLG---FFGGETIGYLDIACSLGPTS 172
QY 169 SYERYG--EFSLPEVAPKIAAWAKRCGERESVAKSLYSPDKVYDFIGLLKKKYGIE 222
Db 173 VIEAFSGVKFLRQETTPGLIKWAERFRAHEAVKP--YMP-TVEEVVAFAKQFENVQ 225

RESULT 5
US-09-765-213A-11
; Sequence 11, Application US/09765213A
; Patent No. US20020079846A1
; GENERAL INFORMATION:
; APPLICANT: Facchini, Peter J
; TITLE OF INVENTION: No. US20020079846A1e1 Glutathione-S-Transferase Nucleic Acids
; TITLE OF INVENTION: Polypeptides and Methods of Use
; FILE REFERENCE: 22542-001
; CURRENT APPLICATION NUMBER: US/09/765,213A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/176708
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Glycine max
US-09-765-213A-11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-653

Query Match 14.7%; Score 172.5; DB 10; Length 286;
Best Local Similarity 28.7%; Pred. No. 4.4e-10;
Matches 58; Conservative 28; Mismatches 107; Indels 9; Gaps 6;

QY 16 PFGQVRVIALAEKGLPYEAEEDLMAGKSDRLLRANPVHKKIPVLLH-DGRAVNESLIIL 74
DB 78 PFAERTLVLLKAGIRHEVINIL-KNKPEWFFKKNP-FGLVPVLENSOGLIYESAITC 135
QY 75 QYLEEAPDPDAPALLSPDYARAQRFWADYVKVYDCGSRMLWKLKGEPOQAQAEMLDI 134
DB 136 EYLDEAYP-GKKLLPDDPYEKACQKMLEFSKVPVSLVGSFIRSONKEDYAGLKEEFKE 194
QY 135 LKTLDGALGDK--PFFGGDKFGFVDAFAFPTAFWHSYERYGEFSLPEVAPKIAAWAKRC 192
DB 195 FTKLEEVLTNNKTTFFGCGNSISIDYILNP---WFERLEAMKUNECVDHTPKLWHAAM 251
QY 193 GERESVAKSLSPDKVYDFIGL 214
DB 252 KEDPTVSALLTSEKDWQGFLEL 273

RESULT 15
US-09-854-133-204
; Sequence 204, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Barin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-854-133-204

Query Match 14.3%; Score 167.5; DB 9; Length 241;
Best Local Similarity 28.6%; Pred. No. 1.2e-09;
Matches 60; Conservative 28; Mismatches 97; Indels 25; Gaps 8;

QY 16 PFGQVRVIALAEKGLPYEAEEDLMAGKSDRLLRANPVHKKIPVLLH-DGRAVNESLIIL 74
DB 33 PFAERTLVLLKAGIRHEVINIL-KNKPEWFFKKNP-FGLVPVLENSOGLIYESAITC 90
QY 75 QYLEEAPDPDAPALLSPDYARAQRFWADYVKVYDCGSRMLWKLKGEPOQAQAEMLDI 134
DB 91 EYLDEAYP-GKKLLPDDPYEKACQKMLEFSKVPVSLVGSFIRSONKEDYAGL 141
QY 135 LK-----TLDGALGDK--PFFGGDKFGFVDAFAFPTAFWHSYERYGEFSLPEVAPK 184
DB 142 LKEEFKEFTKLEEVLTNNKTTFFGCGNSISIDYILNP---WFERLEAMKUNECVDHTPK 198
QY 185 IAAWAKRCGERESVAKSLSPDKVYDFIGL 214
DB 199 LKLMWAAKEDPTVSALLTSEKDWQGFLEL 228

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